```
1    tttaggtgac actatagaat actcaagctt gactaaatat ttagaaagca cattgtgttc
61   agtgaaactt tgtatataat gaatagaata ataaaagatt atgttggatg actagtctgt
121  aattgcctca aggaaagcat acaatgaata agttattttg gtacttcctc aaaatagcca
181  acacaatagg gaaatggaga aaatgtactc tgaacaccat gaaaagggaa cctgaaaatc
241  taatgtgtaa acttggagaa atgacattag aaaacgaaag ctacaaaaga gaacactctt
301  caaaataatc tgagatgcat gaaaggcaaa cattcactag agctggaatt tccctaagtc
361  tatgcaggga taagtagcat atttgacctt caccatgatt atcaagcact tctttggaac
421  tgtgttggtg ctgctggcct ctaccactat cttctctcta gatttgaaac tgattatctt
481  ccagcaaaga caagtgaatc aagaaagttt aaaactcttg aataagttgc aaaccttgtc
541  aattcagcag tgtctaccac acaggaaaaa ctttctgctt cctcagaagt ctttgagtcc
601  tcagcagtac caaaaaggac acactctggc cattctccat gagatgcttc agcagatctt
661  cagcctcttc agggcaaata tttctctgga tggttgggag gaaaaccaca cggagaaatt
721  cctcattcaa cttcatcaac agctagaata cctagaagca ctcatgggac tggaagcaga
781  gaagctaagt ggtactttgg gtagtgataa ccttagatta caagttaaaa tgtacttccg
841  aaggatccat gattacctgg aaaaccagga ctacagcacc tgtgcctggg ccattgtcca
901  agtagaaatc agccgatgtc tgttctttgt gttcagtctc acagaaaaac tgagcaaaca
961  aggaagaccc ttgaacgaca tgaagcaaga gcttactaca gagtttagaa gcccgaggta
1021 ggtggaggga ctagaggact tctccagaca tgattcttca tagagtggta atacaattta
1081 tagtacaatc acattgcttt gattttgtgt atatatatat ttatctgtgt tttaagattg
1141 tgcatattga ccacaattgt ttttattttg taatgtggct ttatatattc tatccatttt
1201 a
```

Figure 1

*MIIKHFFGTVLVLLASTTIFS*LDLKLIIFQQRQVNQESLKLLNKLQTLSIQQ<u>C</u>LPH
RKNFLLPQKSLSPQQYQKGHTLAILHEMLQQIFSLFRA<u>**NIS**</u>LDGWEE<u>**NHT**</u>EK
FLIQLHQQLEYLEALMGLEAEKLSGTLGSDNLRLQVKMYFRRIHDYLENQD
YST<u>C</u>AWAIVQVEISRCLFFVFSLTEKLSKQGRPLNDMKQELTTEFRSPR

Figure 2

IFNα   IFNβ   IFNβ2

Figure 3

```
                          1                                                        70
   IFNB2      (1)  MILKHFFGTVLVLLASTTIFSLDLKLIIFQQRQVNQESLKLLNKLQ-TLSIQQCLPHRKNFLLPQKSLSP
   IFNB       (1)  MTNKCLLQIALLLCFSTTALSMSYNLLGFLQRSSNFQCQKLLWQLNGRLEY--CLKDRMNFDIPEEIKQL
IFNalpha8     (1)  MALTFYLLVALVVLSYKSFSSLGCDLPQTHS-LGNRRALILLAQMR-RISPFSCLKDRHDFEFPQEEFDD
IFNalpha7     (1)  MARSFSLLMVVLVLSYKSICSLGCDLPQTHS-LRNRRALILLAQMG-RISPFSCLKDRHEERFPEEEFDG
IFNalpha6     (1)  MALPFALLMALVVLSCKSSCSLDCDLPQTHS-LGHRRTMMLLAQMR-RISLFSCLKDRHDFRFPQEEFDG
IFNalpha5     (1)  MALPFVLLMALVVLNCKSICSLGCDLPQTHS-LSNRRTLMIMAQMG-RISPFSCLKDRHDFGFPQEEFDG
IFNalpha4b    (1)  MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMG-RISHFSCLKDRHDFGFPEEEFDG
IFNalpha21    (1)  MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMG-RISPFSCLKDRHDFGFPQEEFDG
IFNalpha2     (1)  MALTFALLVALLVLSCKSSVGCDLPQTHS-LGSRRTLMLLAQMR-RISLFSCLKDRHDFGFPQEEF-G
IFNalpha16    (1)  MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLAQMG-RISHFSCLKDRYDFGFPQEVFDG
IFNalpha14    (1)  MALPFALMMALVVLSCKSSCSLGCNLSQTHS-LNNRRTLMLMAQMR-RISPFSCLKDRHDFEFPQEEFDG
IFNalpha13    (1)  MASPFALLMVLVVLSCKSSCSLGCDLPETHS-LDNRRTLMLLAQMS-RISPSSCLMDRHDFGFPQEEFDG
IFNalpha10    (1)  MALSFSLLMAVLVLSYKSICSLGCDLPQTHS-LGNRRALILLGQMG-RISPFSCLKDRHDFRIPQEEFDG
IFNomega1     (1)  MALLFPLLAALVMTSYSPVGSLGCDLPQNHG-LLSRNTLVLLHQMR-RISPFLCLKDRRDFRFPQEMVKG
 IFNgamma     (1)  MKYT-SYILAFQLCIVLGSLGCYCQDPYVKE----AENLKKYFNAG----H--SDVADNGTLF--LGILK
Consensus     (1)  MAL F LLMALLVLS KS CSLGCDLPQTHS L NRR L LLAQM  RISPFSCLKDRHDF FPQEEF

                          71                                                       140
   IFNB2     (70)  QQYQKGHTLAILHEMLQQIFSLFRANISLDGWEENHTEKFLIQLHQQLEYLEALMGLEAEKLSGTLGSDN
   IFNB      (69)  QQFQKEDAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLM
IFNalpha8    (69)  KQFQKAQAISVLHEMIQQTFNLFSTKDSSAALDETLLDEFYIELDQQLNDLESCVMQEVGVIESPLMYED
IFNalpha7    (69)  HQFQKTQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLEACVIQEVGVEETPLMNED
IFNalpha6    (69)  NQFQKAEAISVLHEVIQQTFNLFSTKDSSVAWDERLLDKLYTELYQQLNDLEACVMQEVWVGGTPLMNED
IFNalpha5    (69)  NQFQKAQAISVLHEMIQQTFNLFSTKDSSATWDETLLDKFYTELYQQLNDLEACMMQEVGVEDTPLMNVD
IFNalpha4b   (69)  HQFQKTQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLEACVIQEVGVEETPLMNVD
IFNalpha21   (69)  NQFQKAQAISVLHEMIQQTFNLFSTKDSSATWEQSLLEKFSTELNQQLNDMEACVIQEVGVEETPLMNVD
IFNalpha2    (68)  NQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMKED
IFNalpha16   (69)  NQFQKAQAISAFHEMIQQTFNLFSTKDSSAAWDETLLDKFYIELFQQLNDLEACVTQEVGVEEIALMNED
IFNalpha14   (69)  NQFQKAQAISVLHEMMQQTFNLFSTKNSSAAWDETLLEKFYIELFQQMNDLEACVIQEVGVEETPLMNED
IFNalpha13   (69)  NQFQKAPAISVLHELIQQIFNLFTTKDSSAAWDEDLLDKFCTELYQQLNDLEACVMQEERVGETPLMNAD
IFNalpha10   (69)  NQFQKAQAISVLHEMIQQTFNLFSTEDSSAAWEQSLLEKFSTELYQQLNDLEACVIQEVGVEETPLMNED
IFNomega1    (69)  SQLQKAHVMSVLHEMLQQIFSLFHTERSSAAWNMTLLDQLHTGLHQQLQHLETCLLQVVGEGESAGAISS
 IFNgamma    (58)  NWKEESDRKIMQSQIVSFYKLFKNFKD----DQS-LQKSVETIKEDMN-VKFFNSNKKKRDDFEKLTNY
Consensus    (71)  NQFQKAQAISVLHEMIQQTFNLFSTKDSSAAWDE LLDKF TELYQQLNDLEACV QEVGVEETPLMN D

                          141                                                      210
   IFNB2    (140)  LRLQVKMYFRRIHDYLE-NQDYSTCAWATVQVEISRCLFFVFSLTEKLSKQGRPLNDMKQELTTEFRSPR
   IFNB     (139)  SSLHLKRYYGRILHYLK-AKEYSHCAWTIVRVEILRNFYFINRLTGYLRN------------------
IFNalpha8   (139)  SILAVRKYFQRITLYLT-EKKYSSCAWEVVRAEIMRSFSLSINLQKRLKSKE------------------
IFNalpha7   (139)  FILAVRKYFQRITLYLM-EKKYSPCAWEVVRAEIMRSFSFSTNLKKGLRRKD------------------
IFNalpha6   (139)  SILAVRKYFQRITLYLT-EKKYSPCAWEVVRAEIMRSFSSSRNLQERLRRKE------------------
IFNalpha5   (139)  SILTVRKYFQRITLYLT-EKKYSPCAWEVVRAEIMRSFSLSANLQERLRRKE------------------
IFNalpha4b  (139)  SILAVRKYFQRITLYLT-EKKYSPCAWEVVRAEIMRSLSFSTNLQKRLRRKD------------------
IFNalpha21  (139)  SILAVKKYFQRITLYLT-EKKYSPCAWEVVRAEIMRSFSLSKIFQERLRRKE------------------
IFNalpha2   (138)  SILAVRKYFQRITLYLK-EKKYSPCAWEVVRAEIMRSFSLSTNLQESLRSKE------------------
IFNalpha16  (139)  SILAVRKYFQRITLYLM-GKKYSPCAWEVVRAEIMRSFSFSTNLQKGLRRKD------------------
IFNalpha14  (139)  SILAVKKYFQRITLYLM-EKKYSPCAWEVVRAEIMRSFSFSTNLQKRLRRKD------------------
IFNalpha13  (139)  SILAVKKYFRRITLYLT-EKKYSPCAWEVVRAEIMRSLSLSTNLQERLRRKE------------------
IFNalpha10  (139)  SILAVRKYFQRITLYLI-ERKYSPCAWEVVRAEIMRSLSFSTNLQKRLRRKD------------------
IFNomega1   (139)  PALTLRRYFQGIRVYLK-EKKYSDCAWEVVRMEIMKSLFLSTNMQERLRSKDRDLGSS------------
 IFNgamma   (122)  SVTDLNVQRKAIHELIQVMAELSPAAKTGKR---KRSQML---FRGRRASQ------------------
Consensus   (141)  SILAVRKYFQRITLYL EKKYSPCAWEVVRAEIMRSFS STNLQ RLRRK
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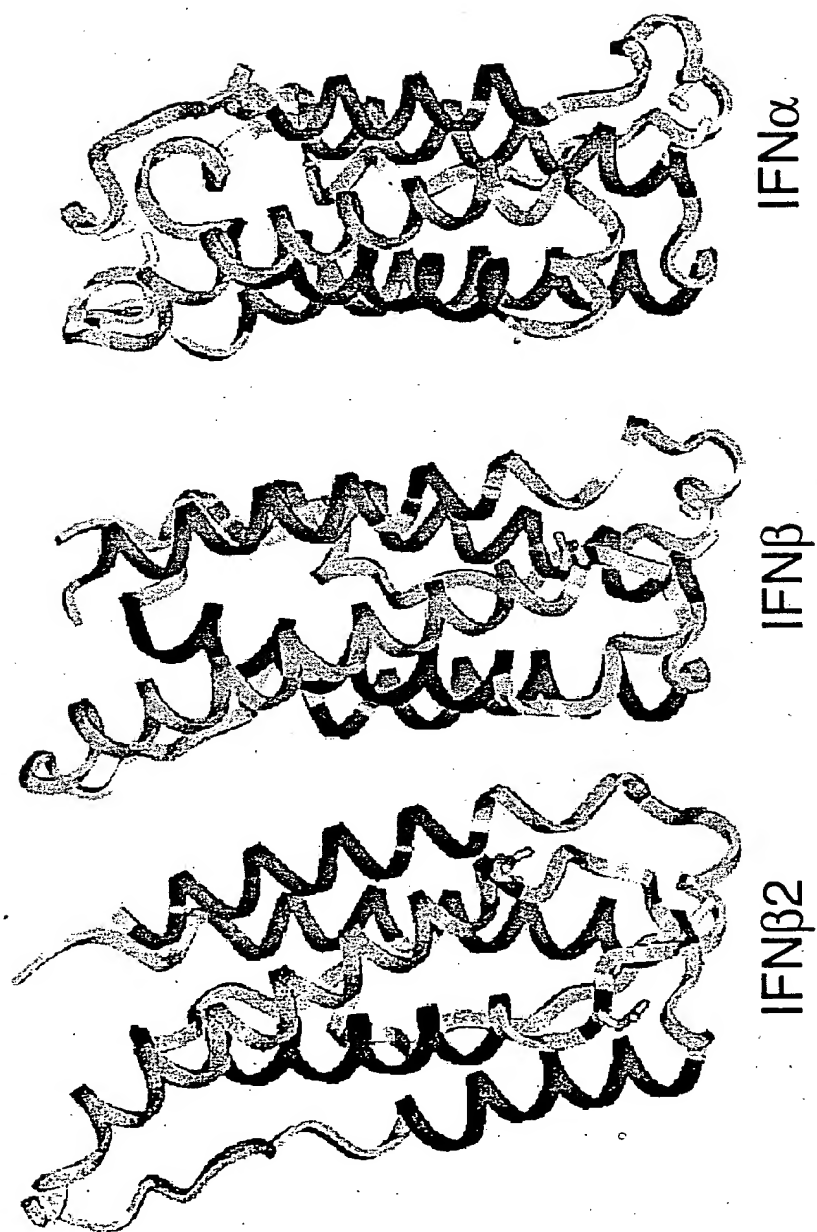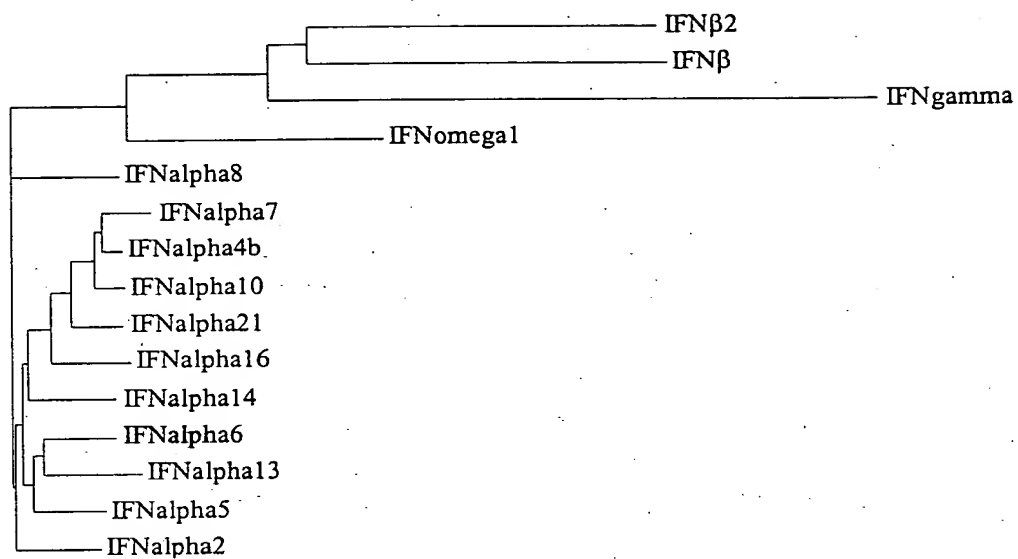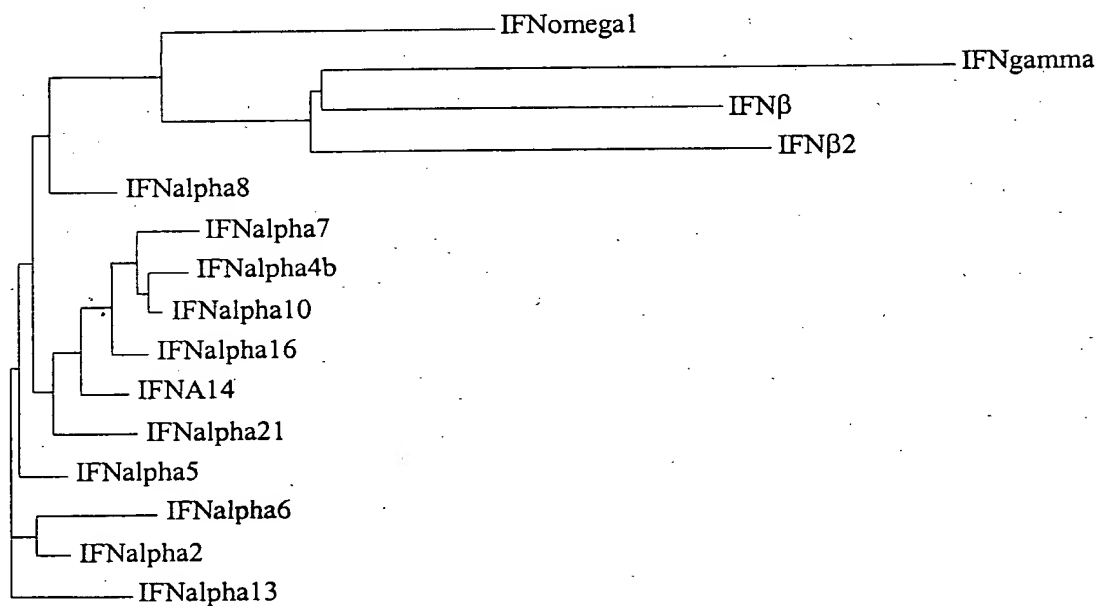
Figure 4

Protein Level Comparison

Nucleotide Level Comparison

Figure 5
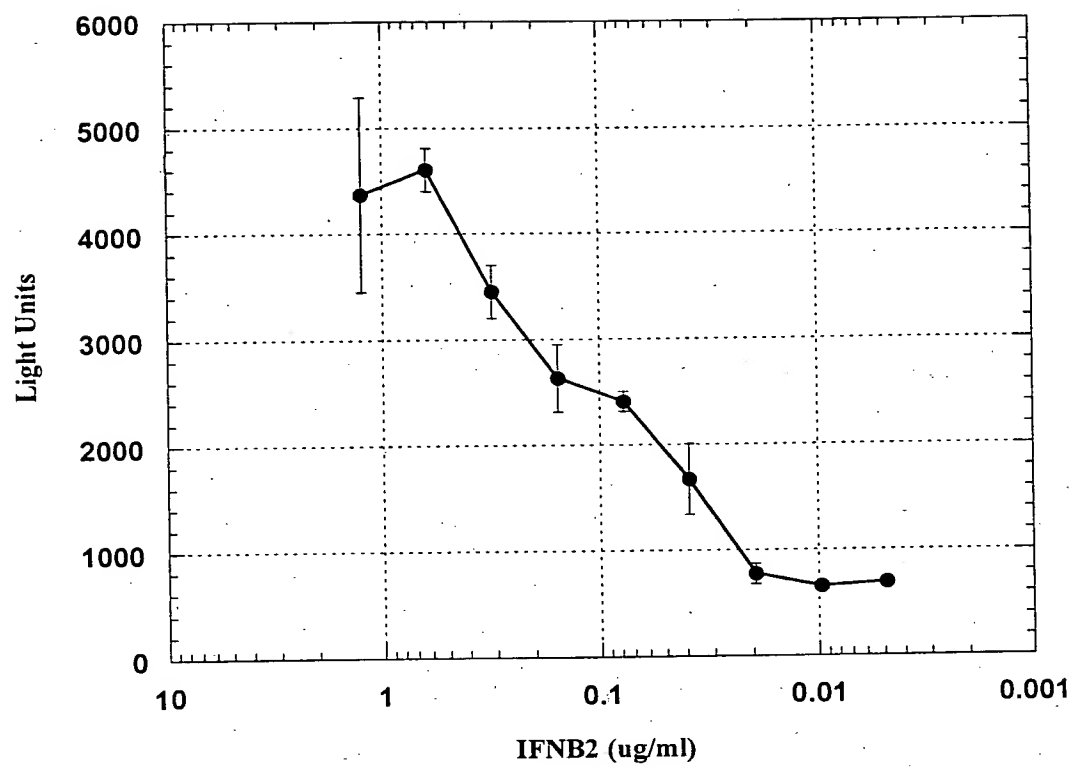
Figure 6

Figure 7

Panel A
HT1080 Cells Stimulated with IFN

Panel B
HT1080IFNAR2c Cells Stimulated with IFN
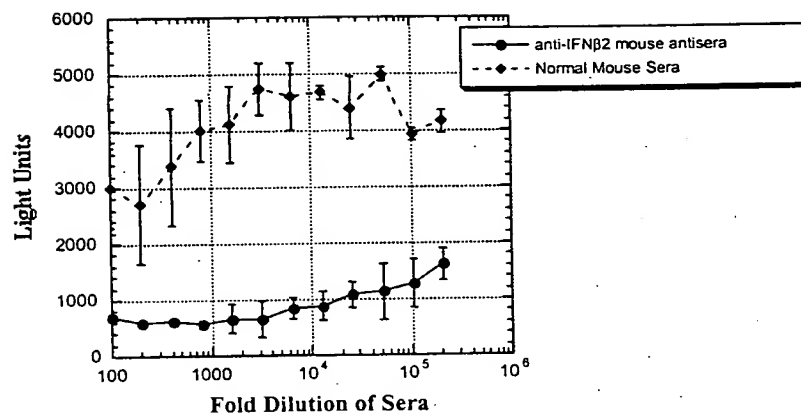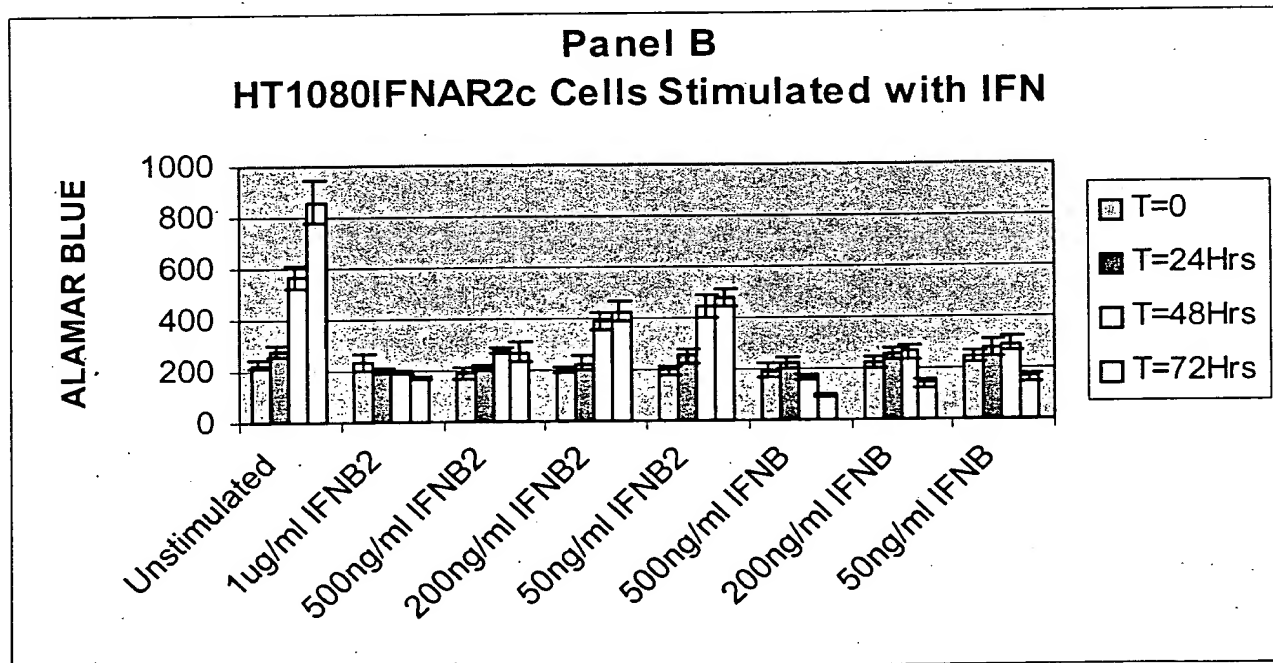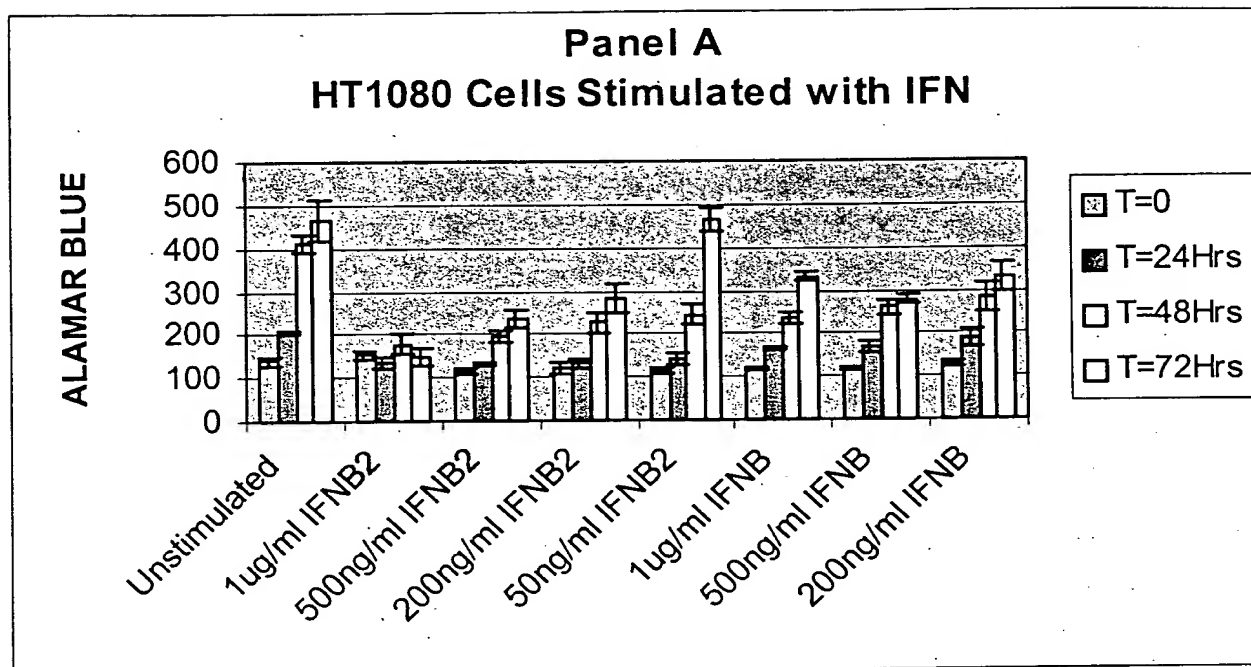
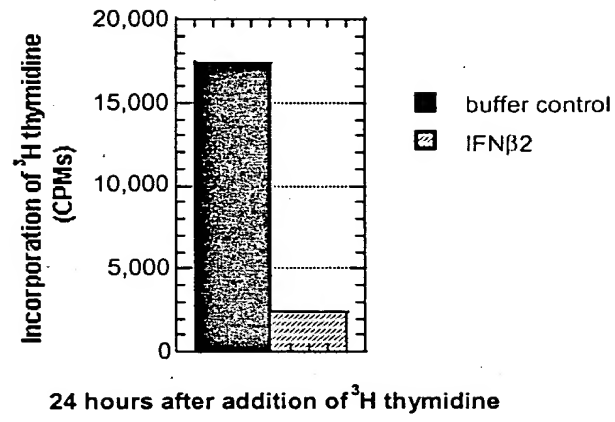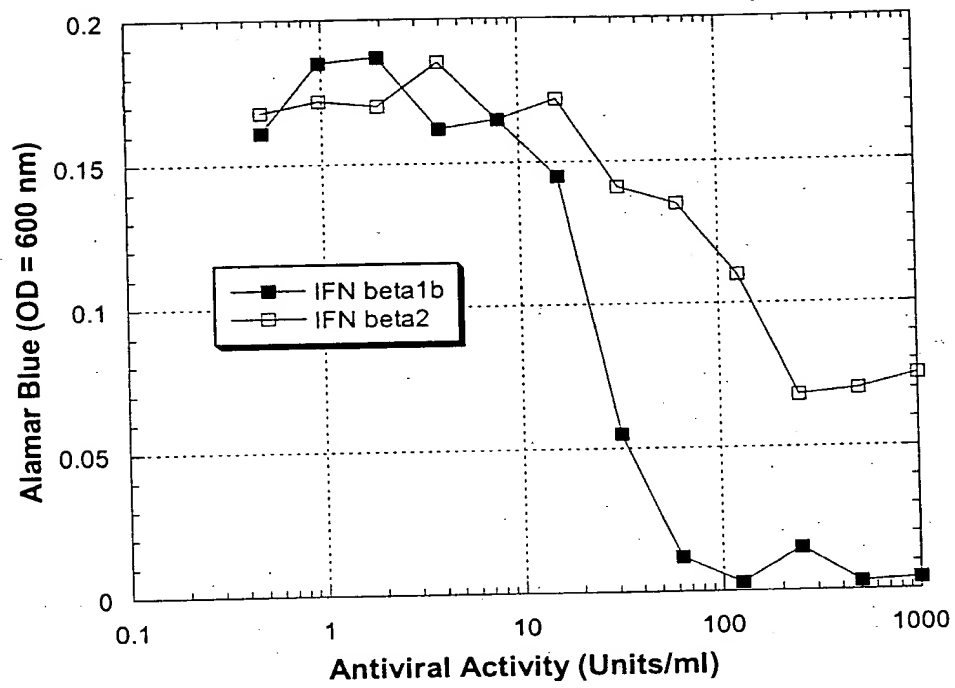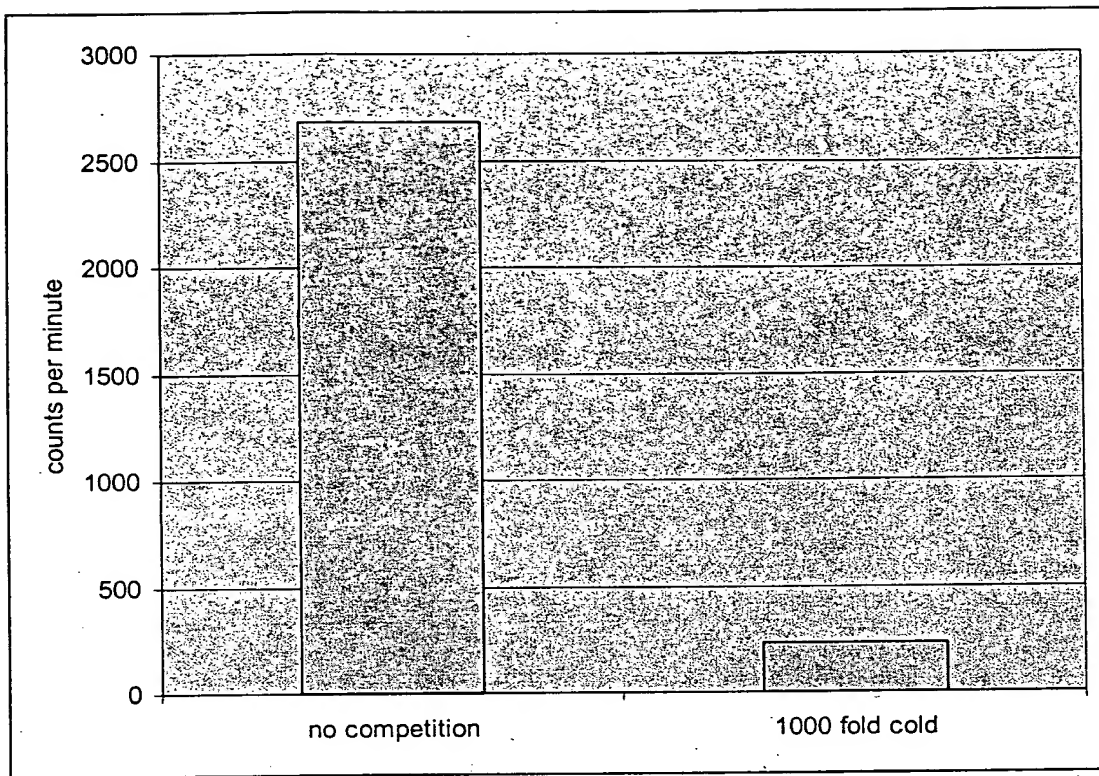**Figure 8**

Figure 9

Figure 10

Figure 11

```
  1   tttaggtgac actatagaat actcaagctt gactaaatat ttagaaagca cattgtgttc
 61   agtgaaactt tgtatataat gaatagaata ataaaagatt atgttggatg actagtctgt
121   aattgcctca aggaaagcat acaatgaata agttattttg gtacttcctc aaaatagcca
181   acacaatagg gaaatggaga aaatgtactc tgaacaccat gaaaagggaa cctgaaaatc
241   taatgtgtaa acttggagaa atgacattag aaaacgaaag ctacaaaaga gaacactctt
301   caaaataatc tgagatgcat gaaaggcaaa cattcactag agctggaatt tccctaagtc
361   tatgcaggga taagtagcat atttgacctt cacc
```

Figure 12

```
361                                              atgatt atcaagcact tctttggaac
421  tgtgttggtg ctgctggcct ctaccactat cttctctcta gatttgaaac tgattatctt
481  ccagcaaaga caagtgaatc aagaaagttt aaaactcttg aataagttgc aaaccttgtc
541  aattcagcag tgtctaccac acaggaaaaa ctttctgctt cctcagaagt ctttgagtcc
601  ttaactgtac caaaaaggac acactctggc cattcttcat gagatgct
```

Figure 13

*MIIKHFFGTVLVLLASTTIFS*LDLKLIIFQQRQVNQESLKLLNKLQTLSIQ
QC̲LPHRKNFLLPQKSLSP

Figure 14

A   B

Brain 1 No Stimulation   Brain 1 EGF Stimulated

C   D

Brain 2 No Stimulation   Brain 2 EGF Stimulated

Figure 15